

1 GAATTGGCC CTCGAGGCCA AGAATTCCGC ACAGAGCGCG GCGCCAGCG CAGGACAGC GCTGTGCGAT CCCGGGCGTC CACCCGCCAT GGGGCTCTCC
 CTTAAACCGG GAGCTCCGGT TCTTAAAGCCG TGCTCCGCGC CGCGGGTCCG GTCCGTCTCG GCACAGCGTA GGGCCCGCAG GTGGCGGGTA CCCCAGAGG
 Me tGlyLeuSer
 1
 101 TGGAGCCCGC GACCTCCACT GCTGATGATC CTGCTACTGG TGCTGTGCTT GTGGCTGCCA CTTGGAGCAG GAAACTCCCT TGCCACAGAG AACAGGTTTG
 ACCTCGGCG CTGGAGGTGA CGACTACTAG GACGATGACC GACGACAGCA CACCGACGGT GAACCTCGTC CTTTGAGGGA ACCTGTCTC TTGTCCAAAC
 5 TrpSerProA rgProProLe uLeuMetile LeuLeuLeuV alleuSerLe uTrpLeuPro LeuGlyAlaG lyAsnSerLe uAlaThrGlu AsnArgPheVal
 201 TGAACAGCTG TACCCAGGCC AGAAGAAAT GCGAGGCTAA TCCTGCTTGC AAGGTGCTT ACCAGCACCT GGGCTCCTGC ACCTCCAGTT TAAGCAGGCC
 ACTTGTCGAC ATGGGTCGG TCTTTCTTTA CGCTCCGATT AGGCGCAACG TTCCGACCGA TGGTCGTGGA CCCGAGGACG TGGAGGTCAA ATTCTGTCGG
 39 AsnSerCy sThrGlnAla ArgLysLysC ysGluAlaAs nProAlaCys LysAlaAlaT yrGlnHisLe uGlySerCys ThrSerSerL euSerArgPro
 301 GCTGCCCTTA GAGGAGTCTG CCATGTCTGC AGACTGCCTA GAGGACAGCAG AACAACTCAG GAACAGCTCT CTGATAGACT GCAGGTGCCA TCGGCGCATG
 CGACGGGAAT CTCCTCAGAC GGTACAGAGG TCTGACGGAT TCTGACGGTCT TGTGTCGAGA GACTATCTGA CGTCCACGGT AGCCGCGTAC
 72 LeuProLeu GluGluSerA laMetSerAl aAspCysLeu GluAlaAlaG luGlnLeuAr gAsnSerSer LeuIleAspC ysArgCysHi sArgArgMet
 401 AAGCACCAG CTACCTGTCT GGACATTTAT TGGACCGTTC ACCCTGCCG AAGCTTGGT GACTACGAGT TGGATGTCTC ACCCTATGAA GACACAGTGA
 TTCGTGTTTC GATGGACAGA CCTGTAATA CTGTTGTTAC ACCTGGCAAG TGGACGGGC TTCGGAACCA CTGATGCTCA ACCTACAGAG TGGGATCTT CTGTGTACT
 105 LysHisGlnA laThrCysLe uAspIleTyr TrpThrValH isProAlaAr gSerLeuGly AspTyrGluL euAspValse rProTyrGlu AspThrValThr
 501 CCAGCAAACC CTGGAATAAT AATCTTAGCA AGTTGAACAT GCTCAAACCA GACTCGGACC TCTGCCTCAA ATTTGCTATG CTGTGTACTC TTCACGACAA
 GGTCTGTTGG GACCTTTTAC TTAGAATCGT TCAACTTGTA CGAGTTTGGT CTGAGCCTGG AGACGGAGTT TAAACGATAC GACACATGAG AAGTGTGTT
 139 SerLysPr oTrpLysMet AsnLeuSerL ysLeuAsnMe tLeuLysPro AspSerAspL euCysLeuLy sPheAlaMet LeuCysThrL euHisAspLys
 601 GTGTGACCGC CTGCGCAAGG CCTACGGGA GGCATGCTCA GGCATCCGT GCCAGCGCA CCTCTGCCTA GCCAGCTGC GCTCCTTCTT TGAGAAGGCA
 CACACTGGCG GACGCGTTCC GGATGCCCTT GGTACGAGT CCGTACGAGT CCGTAGGCGA CCGTCCGCT GGAGACGGT GGAGAGAGAA ACTCTTCCGT
 172 CysAspArg LeuArgLysA laTyrGlyG l ualaCysSer GlyIleArgC ysGlnArgHi sLeuCysLeu AlaGlnLeuA rgSerPhePh eGluLysAla
 701 GCAGAGTCCC AGCTCAGGG TCTGCTGCTG TGTCCCTGTG CACAGAAGA TCGGGGCTGT GGGGAGCGG GCGTAACAC CATCGCCCC AGTTGCGCCC
 CGTCTCAGG TCGAGTCCC AGACGACGAC ACAGGGACAC GTGGTCTTCT ACGCCCGACA CCCCTCGCCG CCGCATTTGT GTAGCGGGG TCAACGCGG
 205 AlaGluSerH isAlaGlnG l yLeuLeuLeu CysProCysa laProGluAs palaGlyCys GlyGluArga rgArgAsnTh rIleAlaPro SerCysAlaLeu
 801 TGCCTTCTGT AACCCCCAAT TGCTTGGATC TGCGGAGCTT TGCCCTGCG GACCTTTTGT GCAGATCAGC CTGTATGGAC TTCCAGACCC ACTGTCTATC
 ACGAAGACA TTGGGGTTA ACGGACCTAG ACGCTCGAA GACGGCACGC CTGGAAACA CGTCTAGTGC GGACTACCTG AAGTCTGGG TGACAGTAGG
 239 ProSerVa lThrProAsn CysLeuAspL euArgSerPh eCysArgAla AspProLeuC ysArgSerAr gLeuMetAsp PheGlnThrH isCysHisPro
 901 TATGACATC CTTGGGACTT GTGCAACTGA GCAGTCCAGA TGTCTGCGG CATACCTGG GCTGATTGG ACTGCCATGA CCCCAACTT CATCAGCAAG
 ATACCTGTAG GAACCTGAA CAGTTGACT CGTCAGGTCT ACAGACGCCC GTATGGACCC CGACTAACCC TGACGGTACT GGGTTTGAA GTAGTCGTTT
 272 MetAspIle LeuGlyThrC ysAlaThrG l uGlnSerArg CysLeuArga laTyrLeuG l yLeuIleGly ThrAlaMetT hrProAsnPh eIleSerLys

FIG. 1A

1001 GTCAACACTA CTGTTGCCCTT AAGCTGCACC TGCCGAGGCA GCGGCAACCT ACAGGACGAG TGTAACAGC GTTCTCCAG AACCCCTGCC
 CAGTTGTGAT GACAACGGAA TTCGACGTGG ACGGCTCCGT CGCCGTGGA TGCTCTGCTC ACACCTGTGC ACCTTTCCAG GAAGAGGGTC TTGGGGACGG
 305 ValAsnThrT hrValAlaLe uSerCysThr CysArgGlys erGlyAsnLe uGlnAspGlu CysGluGlnL eGluArgSe rPheSerGln AsnProCysLeu
 1101 TCGTGGAGGC CATTGCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACAGCAA
 AGCACCTCCG GTAACGTCTGA TTCTACGCAA AGGTGTCTGT CGAGAAGAGG GTCCTGACCC GTCTGAGATG AAAAAAGTCAC CACGTCGTGC TCTTGTCTGT
 339 ValGluAl aileAlaAla LysMetArgP heHisArgG l nLeuPheSer GlnAspTrpA laaspSerTh rPheSerVal ValGlnGlnG l nAsnSerAsn
 1201 CCCTGCTCTG AACTGCAGC CCAGGCTACC CATTTCTTCT TTCTCCATCC TTCCCTTTGAT TCTGCTGCAG ACCCTCTGGT AGCTGGGCTT CCTCAGGGTC
 GGGACGAGAC TCTGACGTCTG GTCCGATGG GTAAGAAAGA AAGAGGTAGG AAGGGAACCTA AGACGACGTC TGGGAGACCA TCGACCCCGAA GGAATCCCCAG
 372 ProAlaLeu ArgLeuGlnP roArgLeuPr oileLeuSer PheSerileL euProLeuL eLeuLeuGln ThrLeuTrp
 1301 CTTTGTCTC TCACACACAC CCAGACTGAT TTGCAGCCTG TGGTGGGAGA GAACTCGCCA GCCTGTGGAA GAAGACGCAG CGTGCTACAC AGCAACCCCGG
 GAAACAGGAG AGGTGGTGTG GGTCCTGACTA AACGTCCGAC ACCACCTCTT CTTGAGCGGT CGGACACCTT CTTCTGCGTC GCACGATGTG TCGTTGGGCC
 1401 AACCAACCAG GCATTCGCA GCACATCCG TCTGCTCCAG AAGAGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGGCTAG TTTTCAAAAC
 TTGGTTGGTC CGTAAGGCGT CGTGTAGGCG AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AAGGCTAGGA CTGCGCCGATC AAAAGTTTGG
 1501 TCCCTTGCCC CTGCTTCCTT CTGGCTCAGG CTGCTCCTCC TTAGGACTTT GTGGGTCCAG TTTTGCCTTC TGTTCTGATG GTGATTAGCG GCTCACCTCC
 AGGGAACGGG GACGAAGGAA GACCGAGTCC GACGAGGAGG AATCCTGAAA CACCCAGGTC AAACCGAAG ACAAGACTAC CACTAATCGC CGAGTGGAGG
 1601 AGCGCTTCTT CCTGTCTTCCC AGGACCAACC AGAGGCTAAG GAATCAGTCA TTCCCTGTTG CCTTCTCCAG GAAGGCAGGC TAAGGGTTCT GAGGTGACTG
 TCGCGAAGAA GGACAAAGGG TCCTGGTGGG TCCTCCGATTC CTTAGTCACT AAGGGACAAC GGAAGAGGTC CTTCCGTCGG ATTCCCCAGA CTCCACTGAC
 1701 AGAAAAATGT TTCTTTTGTG TGAAGGCTG GTGCTCCAGC CTCACGTC CTCTGAATGG AAGATAAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC
 TCTTTTACAA AAGGAAACAC ACCTTCCGAC CACGAGGTCTG GAGGTGACG GAGACTTACC TTCTATTTTT GGACGACAC AGAACTGACG AGACGGTCCG
 1801 AATCCTGAAC ATTTGGGCAT GAAGAGCTAA AGTCTTTTGG TCTTGTTTAA CTCCTATTAC TGTCCCCAAA TTCCCCCTAGT CCCTTGGGTC ATGATTAAAC
 TTAGGACTTG TAAACCCGTA CTTCTCGATT TCAGAAACCC AGAACAAATT GAGGATAATG ACAGGGGTTT AAGGGGATCA GGGAAACCCAG TACTTAATTG
 1901 ATTTTGACTT AAAAAAAA AAAAAAAA AAAAAA
 TAAAACTGAA TTTTTTTTTT TTTTTTTTTT TTTTTT

FIG. 1B

463	S	L	A	E	T	S
392	L	L	Q	T	L	W

hGFra3	1	M	V	R	P	L	N	P	R	P	L	P	P	V	V	L	M	L	L	L	L	P	P	S	P	L	P	L	A	G	D	P	L	P	T	E	S	R	L	M	N	S	C	L	Q	A	R	R	K		
mGFra3	1	-	-	M	G	L	S	W	S	P	R	P	P	L	L	M	I	L	L	L	V	L	S	L	W	-	L	P	L	G	A	G	N	S	L	A	T	E	N	R	F	V	N	S	C	T	Q	A	R	K	K

hGFra3	51	C	Q	A	D	P	T	C	S	A	A	Y	H	L	D	S	C	T	S	S	I	S	T	P	L	S	E	E	P	S	V	P	A	D	C	L	E	A	A	Q	L	R	N	S	S	L	I	G			
mGFra3	48	C	E	A	N	P	A	C	K	A	A	Y	Q	H	L	G	S	C	T	S	S	L	S	R	P	L	P	L	E	E	S	A	M	S	A	D	C	L	E	A	A	E	Q	L	R	N	S	S	L	I	D

hGFra3	101	C	M	C	H	R	R	M	K	N	Q	V	A	C	L	I	Y	W	T	V	H	R	A	R	S	L	G	N	Y	E	L	D	V	S	P	Y	E	D	T	V	T	S	K	P	W	K	M	N	L	S
mGFra3	98	C	R	C	H	R	R	M	K	H	Q	A	T	C	L	I	Y	W	T	V	H	P	A	R	S	L	G	D	Y	E	L	D	V	S	P	Y	E	D	T	V	T	S	K	P	W	K	M	N	L	S

hGFra3	151	K	L	N	M	L	K	P	D	S	D	L	C	L	K	F	A	M	L	C	T	L	N	D	K	C	D	R	L	R	K	A	Y	G	E	A	C	S	G	P	H	C	Q	R	H	V	C	L	R	Q	L
mGFra3	148	K	L	N	M	L	K	P	D	S	D	L	C	L	K	F	A	M	L	C	T	L	H	D	K	C	D	R	L	R	K	A	Y	G	E	A	C	S	G	I	R	C	Q	R	H	L	C	L	A	Q	L

hGFra3	201	L	T	F	F	E	K	A	A	E	P	H	A	Q	G	L	L	C	P	C	A	P	N	D	R	G	C	G	E	R	R	R	N	T	I	A	P	N	C	A	L	P	P	V	A	P	N	C	L	E
mGFra3	198	R	S	F	F	E	K	A	A	E	S	H	A	Q	G	L	L	C	P	C	A	P	E	D	A	G	C	G	E	R	R	R	N	T	I	A	P	S	C	A	L	P	S	V	T	P	N	C	L	D

hGFra3	251	L	R	R	L	C	F	S	D	P	L	C	R	S	R	L	V	D	F	Q	T	H	C	H	P	M	D	I	L	G	T	C	A	T	E	Q	S	R	C	L	R	A	Y	L	G	L	I	G	T	A	M
mGFra3	248	L	R	S	F	C	R	A	D	P	L	C	R	S	R	L	M	D	F	Q	T	H	C	H	P	M	D	I	L	G	T	C	A	T	E	Q	S	R	C	L	R	A	Y	L	G	L	I	G	T	A	M

hGFra3	301	T	P	N	F	V	S	N	V	N	T	S	V	A	L	S	C	T	C	R	G	S	G	N	L	Q	E	E	C	E	M	L	E	G	F	F	S	H	N	P	C	L	T	E	A	I	A	A	K	M	R
mGFra3	298	T	P	N	F	I	S	K	V	N	T	T	V	A	L	S	C	T	C	R	G	S	G	N	L	Q	E	C	E	Q	L	E	R	S	F	S	Q	N	P	C	L	V	E	A	I	A	A	K	M	R	

hGFra3	351	F	H	S	Q	L	F	S	Q	D	W	P	H	P	T	F	A	V	M	A	H	Q	N	E	N	P	A	V	R	P	Q	P	W	V	P	S	L	F	S	C	T	L	P	L	I	L	L	S	L	W
mGFra3	348	F	H	R	Q	L	F	S	Q	D	W	A	D	S	T	F	S	V	V	Q	Q	N	S	N	P	A	L	R	L	Q	P	R	L	P	I	L	S	F	S	I	L	P	L	I	L	L	Q	T	L	W

FIG. 3

48613 1 MVRPLNPRPLPPVVLMLLLPPSPPLAAGDPLPTESRLMNSCLQARRK
48614 1 MVRPLNPRPLPPVVLMLLLPPSPPLAAGDPLPTESRLMNSCLQARRK

48613 51 CQADPTCSAAYHHLDSDCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48614 51 CQADPTCSAAYHHLDSDCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG

48613 101 CMCHRRMKNQVACLDIYWTVHRRARSLGNYELDVSPYEDTVTSKPWKMNLS
48614 101 CMCHRRMKNQVACLDIYWTVHRRARSL

48613 151 KLNMLKP DSDLCLKFAMLCCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL
48614 127 DSDLCLKFAMLCCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL

48613 201 LTFEKEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
48614 170 LTFEKEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE

48613 251 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTATEQSRCLRAYLGLIGTAM
48614 220 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTATEQSRCLRAYLGLIGTAM

48613 301 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR
48614 270 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR

48613 351 FHSQLFSQDWPHPPTFAVMAHQENENPAVRPQPWPVPSLFSCTLPLILLSLW
48614 320 FHSQLFSQDWPHPPTFAVMAHQENENPAVRPQPWPVPSLFSCTLPLILLSLW

FIG. 4

DNA48613.orf	1	A	T	G	G	T	G	C	G	C	C	C	C	T	G	A	C	C	G	C	G	A	C	C	G	C	T	G	A	T	G	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T	C	T	T
--------------	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

FIG. 5A

DNA48613.orf	398	TCTCCCCCTATGAAG.....ACACAGTGACCAGC
GENFRa1.orf	356	CCC CATATGAACCAAGTTA.....ACAGCAGATTGTCA
GENFRa2.orf	374	CCTCCCCCTATGAAGCCGGTGACCTCCCGCCTCTCGGACATCTTCAAGGCTT
DNA48613.orf	427	AAACCTGGAAAAATGAATCTCAGCAAACTGAACAATGCTCAACCAAGACTC
GENFRa1.orf	388	GATATATTCCGGGTGGTCCCATTTCAATATCAGTGGAGCAATCCCAAAGG
GENFRa2.orf	424	GCTTCAATCTTCTCAGGGAACAAGGGCAAGACCCGGTGTCAAGCCAAAGAG
DNA48613.orf	477	AGACCTCTGCCTCAAGTTTGCCAATGCTGTACTCTCAATGACAAAGTGTG
GENFRa1.orf	438	GAACAACCTGCCTGGATGCAAGCGAAGGCCCTGCAACCTCGACGACATTTGCA
GENFRa2.orf	474	CAACCAATTGCCCTGGATGCTGCCAAGGCCCTGCAACCTGAATGACAACTTGCA
DNA48613.orf	527	ACCGGCTGCGGCAAGGCCCTACGGGGAGGCGTGCTCCGGGCGCCCACTG...C
GENFRa1.orf	488	AGAAGTACAAGTTCGGCGTACATCAACCCCGTGCAACCAAGTGTCT...C
GENFRa2.orf	524	AGAACTGCGGCTCTCCTACATCTCCATCTGCAACCGCGAGATCTCGCC
DNA48613.orf	574	CAGCGCCACAGTCTGCTCAGGCAAGCTGCTCACTTTCTTCGAGAGAGGCGCGC
GENFRa1.orf	535	AATGATGTCTGCAACCGCCGCAAGTGCCACAAGGCCCTCCGGCAGTTCTT
GENFRa2.orf	574	ACCGAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGCGCAGTTCTT
DNA48613.orf	624	CGAG.....CCCAACGCGCAGGCGCTGCTACTGTGCCCATGTGCCCCCA
GENFRa1.orf	585	TGACAAAGGTCCCGGCCAAGCACAGCTACGGAATGCTCTTCTGCTCCTGCC
GENFRa2.orf	624	CGACCGGGTGCCCAAGCGAGTACACTACCGCATGCTCTTCTGCTCCTGCC
DNA48613.orf	668	ACGACC GG GCTGCGGGGAGCGCCGGCGCAACCAATCGCCCAACTGCTG
GENFRa1.orf	635	GGGACATCGCCTGCAACAGAGCGGAGGCGGACAGCAATCGTGCCCTGTGTGC
GENFRa2.orf	674	AGACCAGGCGTGCGCTGAGCGCCGCGCGGCAACCATCTCTGCCCAAGCTGC

FIG. 5B

DNA48613.orf	718	G	C	G	C	T	G	C	C	...	G	C	C	T	G	T	G	C	C	C	C	C	A	A	C	T	G	C	C	T	G	G	A	G	C	T	G	C	G	G	C	G	C	T	C	T	G						
GENFRa1.orf	685	T	C	C	T	A	T	G	A	G	A	G	A	G	A	G	C	C	C	A	A	C	T	G	T	T	G	A	A	T	T	G	C	A	G	G	A	C	T	C	C	T	G	C	T	G							
GENFRa2.orf	724	T	C	C	T	A	T	G	A	G	G	A	C	A	A	G	G	A	A	C	C	C	A	A	C	T	G	C	C	T	G	G	A	C	T	G	C	G	T	G	G	C	G	T	G	T	G						
DNA48613.orf	765	C	T	T	C	T	C	G	A	C	C	G	C	T	T	T	G	C	A	G	A	T	C	A	C	G	C	C	T	G	G	A	T	T	T	C	C	A	G	A	C	C	C	A	C	T							
GENFRa1.orf	735	C	A	A	G	A	C	G	A	A	T	T	A	C	A	T	C	T	G	C	A	G	A	T	C	T	C	G	C	C	T	T	G	C	G	G	A	T	T	T	T	T	A	C	C	A	A	C	T				
GENFRa2.orf	774	C	C	G	A	C	T	G	A	C	C	A	C	T	G	T	C	G	G	T	C	C	G	G	C	T	G	G	C	C	T	G	G	A	C	A	T	T	C	C	A	T	T	G	C	C	A	A	T				
DNA48613.orf	815	G	C	C	A	T	C	C	A	T	G	A	C	A	T	C	T	A	G	G	A	C	T	T	G	T	G	C	A	A	C	A	G	A	G	C	A	G	T	C	A	G	A	...									
GENFRa1.orf	785	G	C	C	A	G	C	C	A	G	A	T	C	A	G	T	C	T	G	T	C	A	G	C	A	G	T	C	T	A	A	G	G	A	A	A	C	T	A	C	G	C	T										
GENFRa2.orf	824	G	T	C	G	A	G	C	C	T	C	C	T	A	C	C	A	G	A	C	G	G	T	C	A	C	C	A	G	C	T	G	C	C	T	G	C	G	G	A	C	A	A	T	T	A	C	C	A	G			
DNA48613.orf	862	...	T	G	T	C	T	A	C	G	A	G	C	A	T	A	C	T	G	G	G	G	C	T	G	A	T	T	G	G	A	C	T	G	C	A	T	G	A	C	C	C	C	C	C	A	A						
GENFRa1.orf	835	G	A	C	T	G	C	T	C	C	T	C	G	C	T	A	C	T	C	G	G	G	C	T	A	T	T	G	C	A	C	A	G	T	C	A	T	G	A	C	C	C	C	C	C	A	A						
GENFRa2.orf	874	G	C	G	T	G	T	C	T	G	G	G	C	T	C	T	T	A	T	G	C	T	G	G	C	A	T	G	A	T	T	G	G	T	T	G	A	C	A	T	G	A	C	A	C	C	T	A	A				
DNA48613.orf	909	C	T	T	T	G	T	C	A	G	C	A	A	T	G	T	C	A	...	A	C	A	C	C	A	G	T	G	C	C	T	T	A	A	G	C	T	G	C	A	C	T											
GENFRa1.orf	885	C	T	A	C	A	T	A	G	A	C	T	C	C	A	G	T	A	...	G	C	C	T	C	A	G	T	G	T	G	G	C	C	C	C	A	T	G	G	T	G	A	C	T									
GENFRa2.orf	924	C	T	A	T	G	T	G	G	A	C	T	C	C	A	G	C	C	C	C	A	C	T	G	G	C	A	T	C	G	T	G	T	G	T	C	C	C	C	T	G	G	T	G	C	A	G	C	T				
DNA48613.orf	953	G	C	C	G	A	G	C	A	G	T	G	G	C	A	A	C	T	G	C	A	G	G	A	G	G	A	G	T	G	A	A	A	T	G	C	T	G	G	A	A	G	G	T	T	C							
GENFRa1.orf	929	G	C	A	G	C	A	C	A	G	T	G	G	G	A	A	C	G	A	C	C	T	A	G	A	G	A	G	T	G	C	T	T	G	A	A	T	T	C	T	T	G	A	A	T	T	C						
GENFRa2.orf	974	G	T	C	G	T	G	G	C	A	G	C	G	G	G	A	A	C	A	T	G	G	A	G	G	A	G	T	G	A	G	A	A	G	T	T	C	C	T	C	A	G	G	G	A	C	G						
DNA48613.orf	1003	T	T	C	T	C	C	C	A	C	A	A	C	C	C	C	T	G	C	C	T	C	A	C	G	A	G	C	C	A	T	T	G	C	A	G	C	T	A	A	G	A	T	G	C	G	T	T					
GENFRa1.orf	979	T	T	C	A	A	G	C	A	A	T	A	C	A	T	G	T	C	T	T	A	A	A	A	T	G	C	A	T	T	C	A	A	G	C	C	T	T	T	G	G	C	A	A	T	G	G	C	A	A	T	G	
GENFRa2.orf	1024	T	T	C	A	C	C	G	A	G	A	C	C	C	A	T	G	C	C	T	C	G	G	A	A	C	G	C	C	A	T	C	A	G	G	C	C	T	T	T	G	G	C	A	A	C	G	G	C	A	A	T	G

FIG. 5C

DNA48613.orf 1053 T C A C A G C C A A C T C T T C T C C C A G G A C T G C C A C A C C C T A C C T T T G C T G T G A
 GENFRa1.orf 1029 C T C C G A T G T G A C C G T G T G G C A G C C A G C C T T C C C A G T A C A G A C C A C C A C T G
 GENFRa2.orf 1074 C A C G G A C G T G A A C G T G T C C C C A A A G G C C C C T C G T T C A G G C C A C C C A G G

 DNA48613.orf 1103 T G G C C A C A C C A G A A T G A A A A C C C T G C T G T G A G G C C A C A G C C C T G G G T G C C C
 GENFRa1.orf 1079 C C A C T A C C A C C A C T G C C C T C C G G G T T A A G A A C A A A C C C C T G G G C C A G C A
 GENFRa2.orf 1124 C C C C T C G G G T G G A G A G A C G C C T T C T T T G C C A G A T G A C C T C A G T G A C A G T

 DNA48613.orf 1153 T C T C T T T T C C C T G C A C G C T T C C C T T G A T T C T G C T C C T G A G C C T A T G G T A
 GENFRa1.orf 1129 G G G T C T G A G A A T G A A A T T C C C A C T C A T G T T T T G C C A C C G T G T G C A A A T T T
 GENFRa2.orf 1174 A C C A G C T T G G G A C C A G T G T C A T C A C C A C C T G C A C G T C T G T C C A G G A G C A

 DNA48613.orf 1203 G
 GENFRa1.orf 1179 A C A G G C A C A G A A G C T G A A A T C C A A T G T G T C G G G C A A T A C A C A C C T C T G T A
 GENFRa2.orf 1224 G G G G C T G A A G G C C A C A A C T C C A A A G A G T A A G C A T G T G C T T C A C A G A G C

 GENFRa1.orf 1229 T T T C C A A T G G T A A T T A T G A A A A G A A G G T C T C G G T G C T T C C A G C C A C A T A
 GENFRa2.orf 1274 T C A C G A C A A A T A T C A T C C C A G G G A G T A A C A A G T G A T C A A A C C T A A C T C A

 GENFRa1.orf 1279 A C C A C A A A T C A A T G G C T G C T C C T C C A A G C T G T G G T C T G A G C C C A C T G C T
 GENFRa2.orf 1324 G G C C C A G C A G A G C C A G A C C G T C G G C T G C C T T G A C C G T G C T G T C T G C C T

 GENFRa1.orf 1329 G G T C C T G G T G G T A A C C G C T C T G T C C A C C C T A T T A T C T T T A C A G A A A C A T
 GENFRa2.orf 1374 G A T G C T G A A A C A G G C C T T G T A G

 GENFRa1.orf 1379 C A T A G

FIG. 5D

REPLACEMENT SHEET

[illegible]

FIG. 6

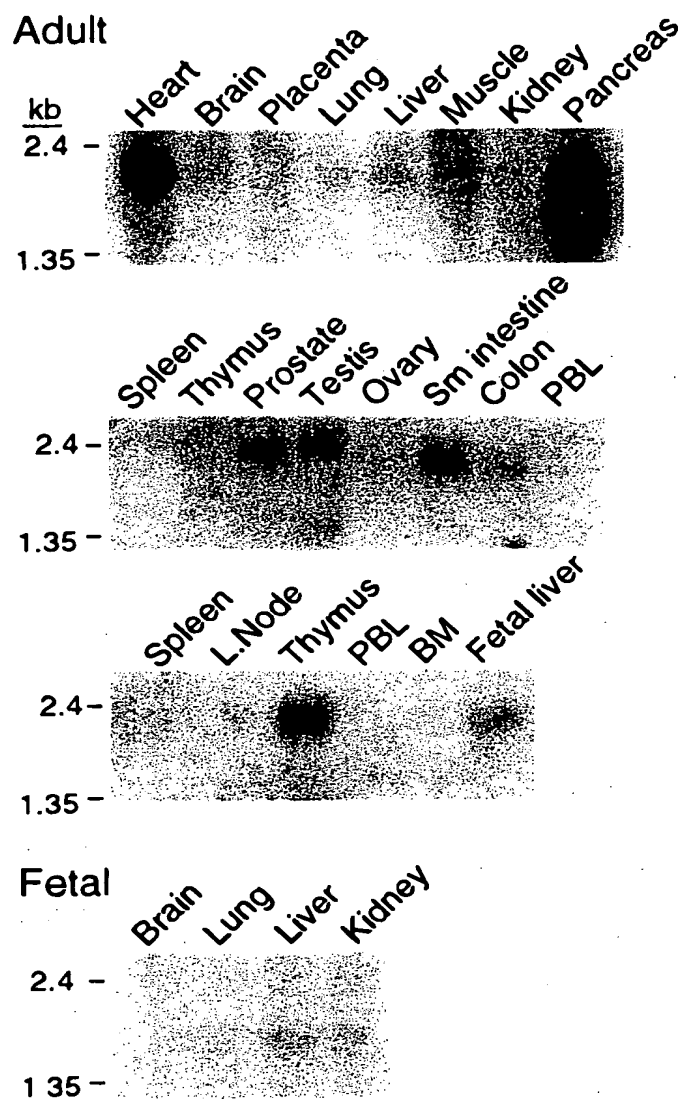


FIG. 7

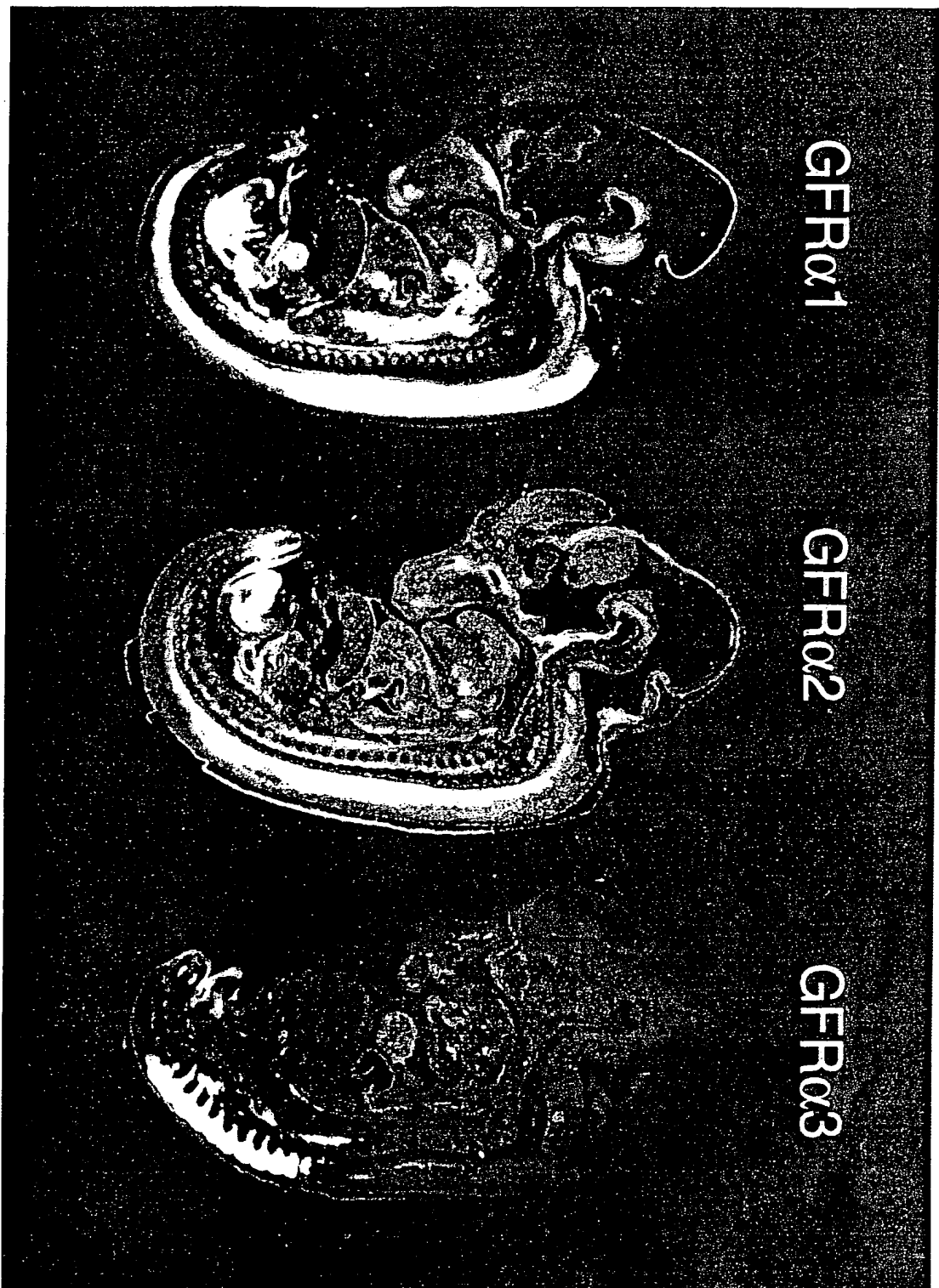
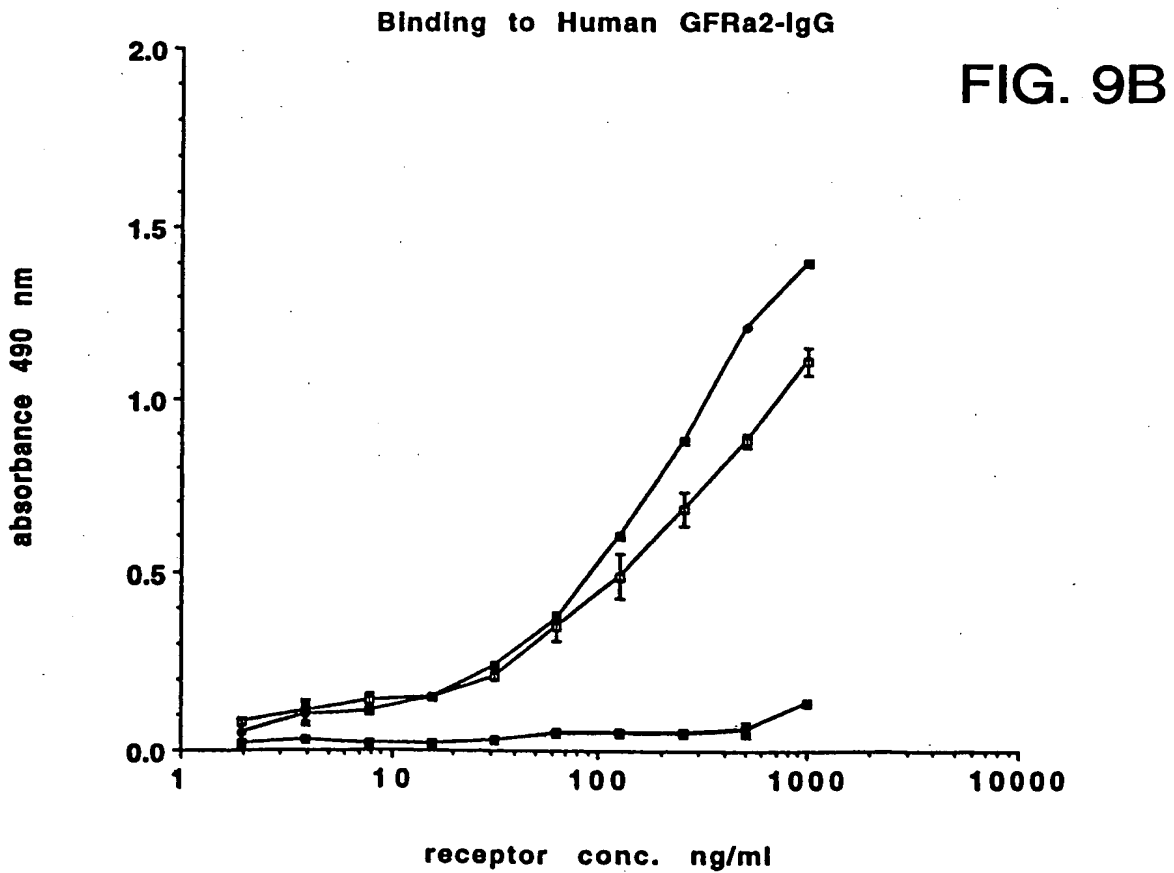
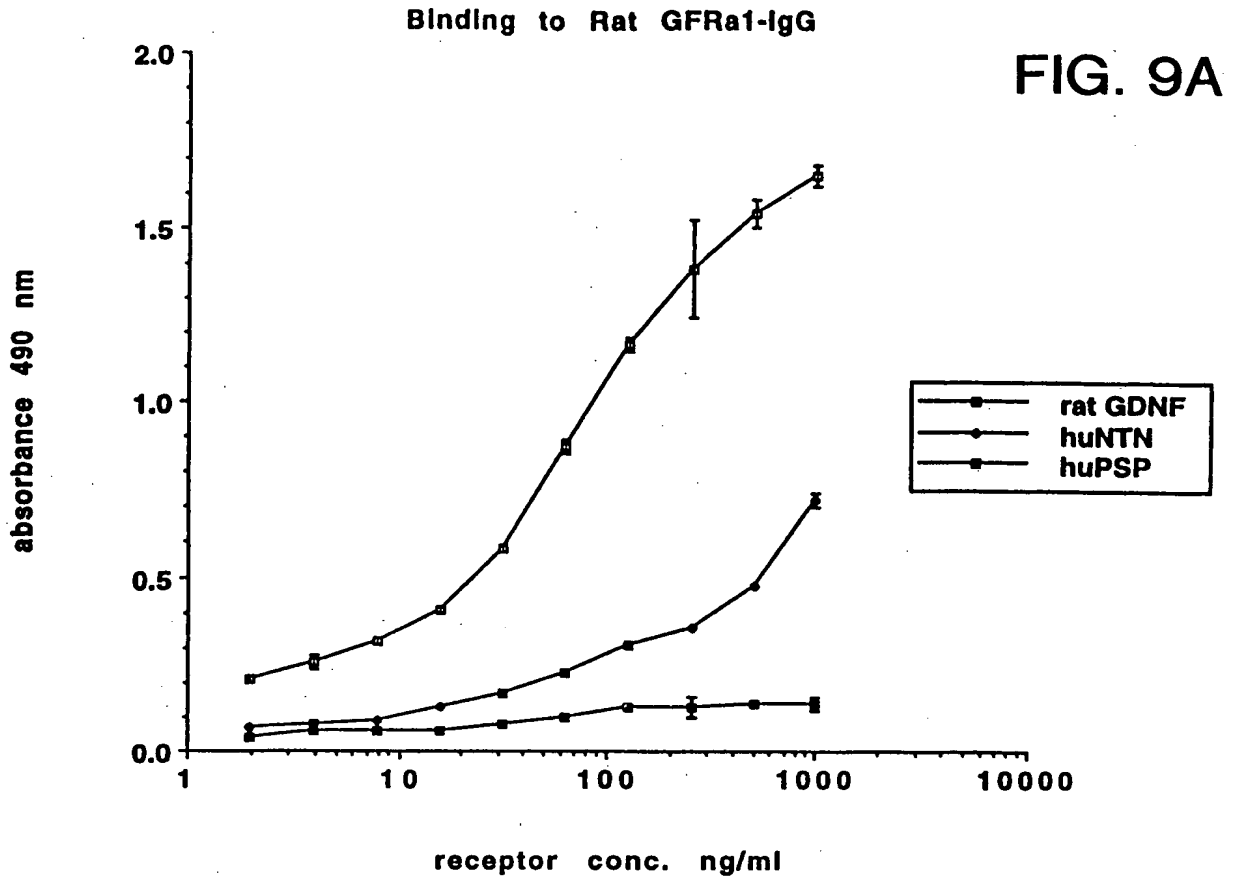
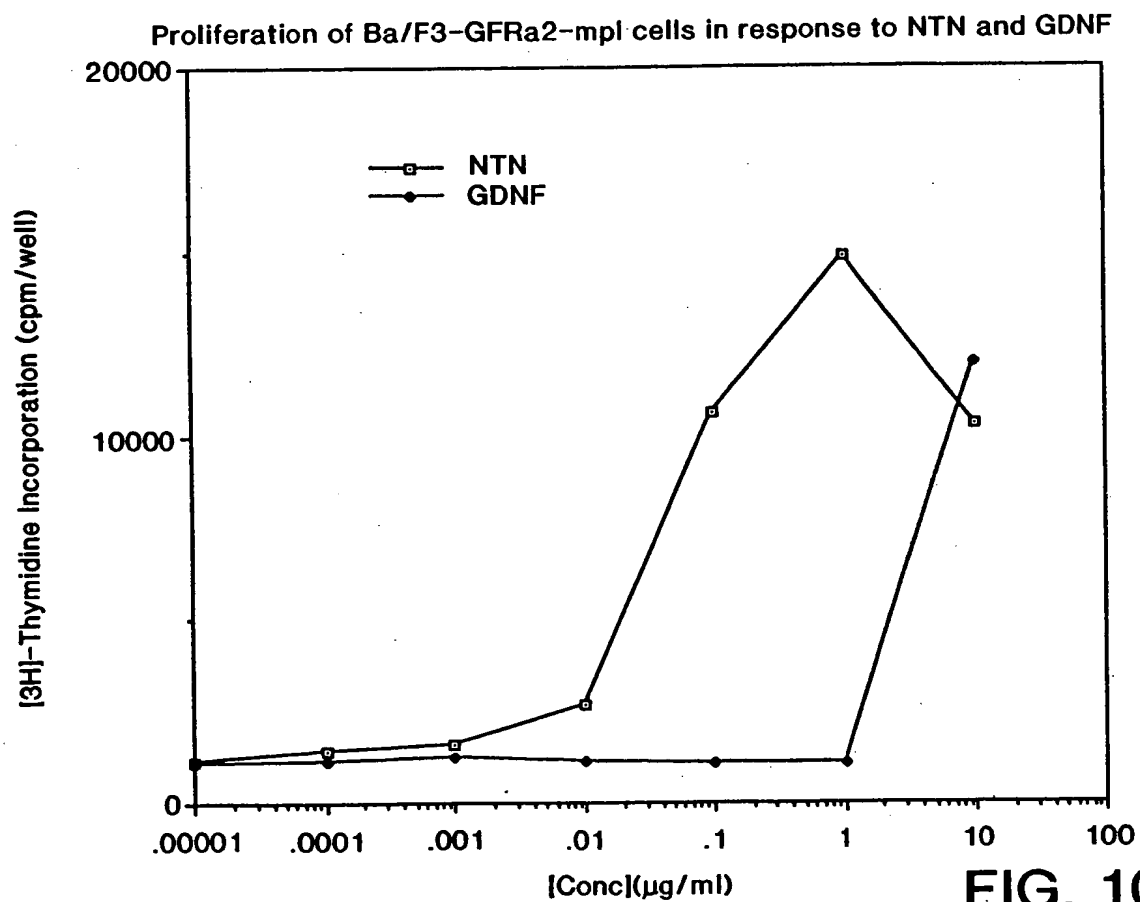
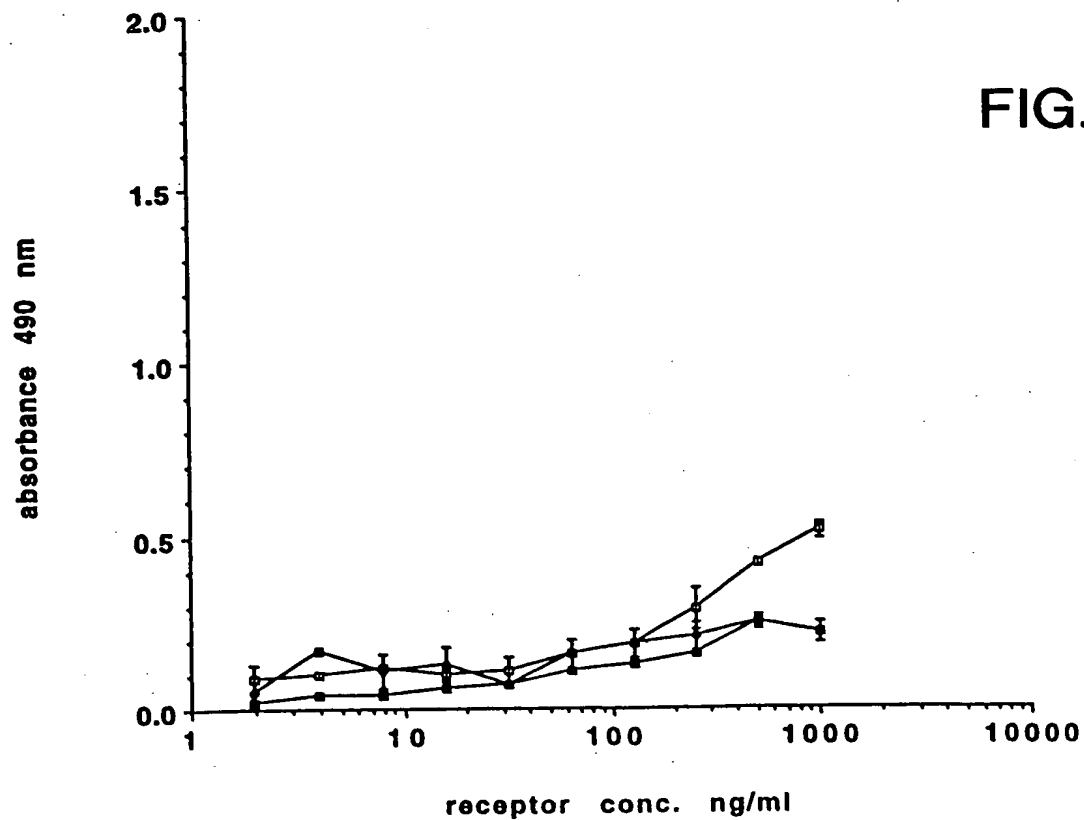


FIG. 8



Binding to Human GFRa3-IgG



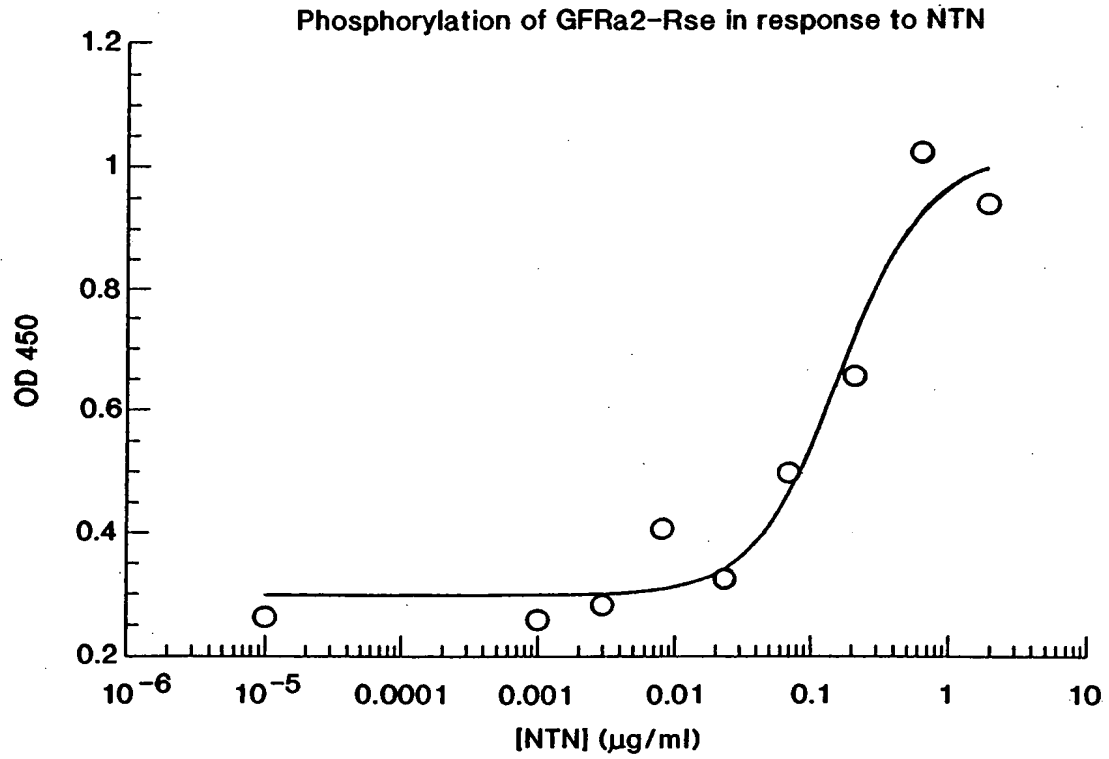


FIG. 11

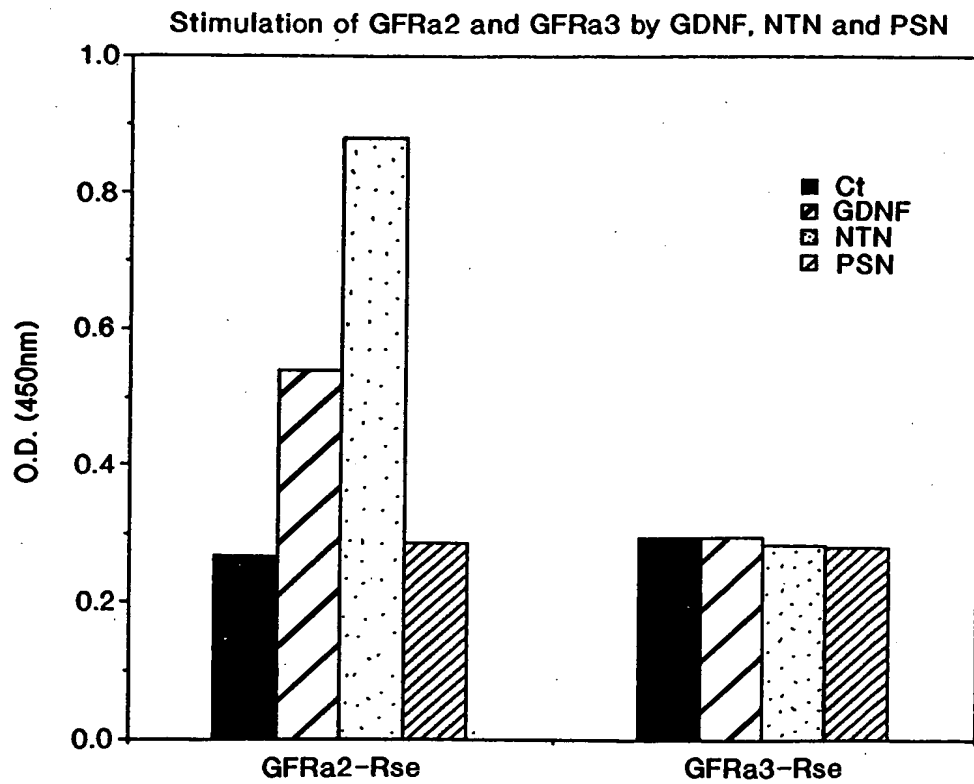


FIG. 12

Agonistic activity of anti gD mAbs in gD-alpha2-rse KIRA

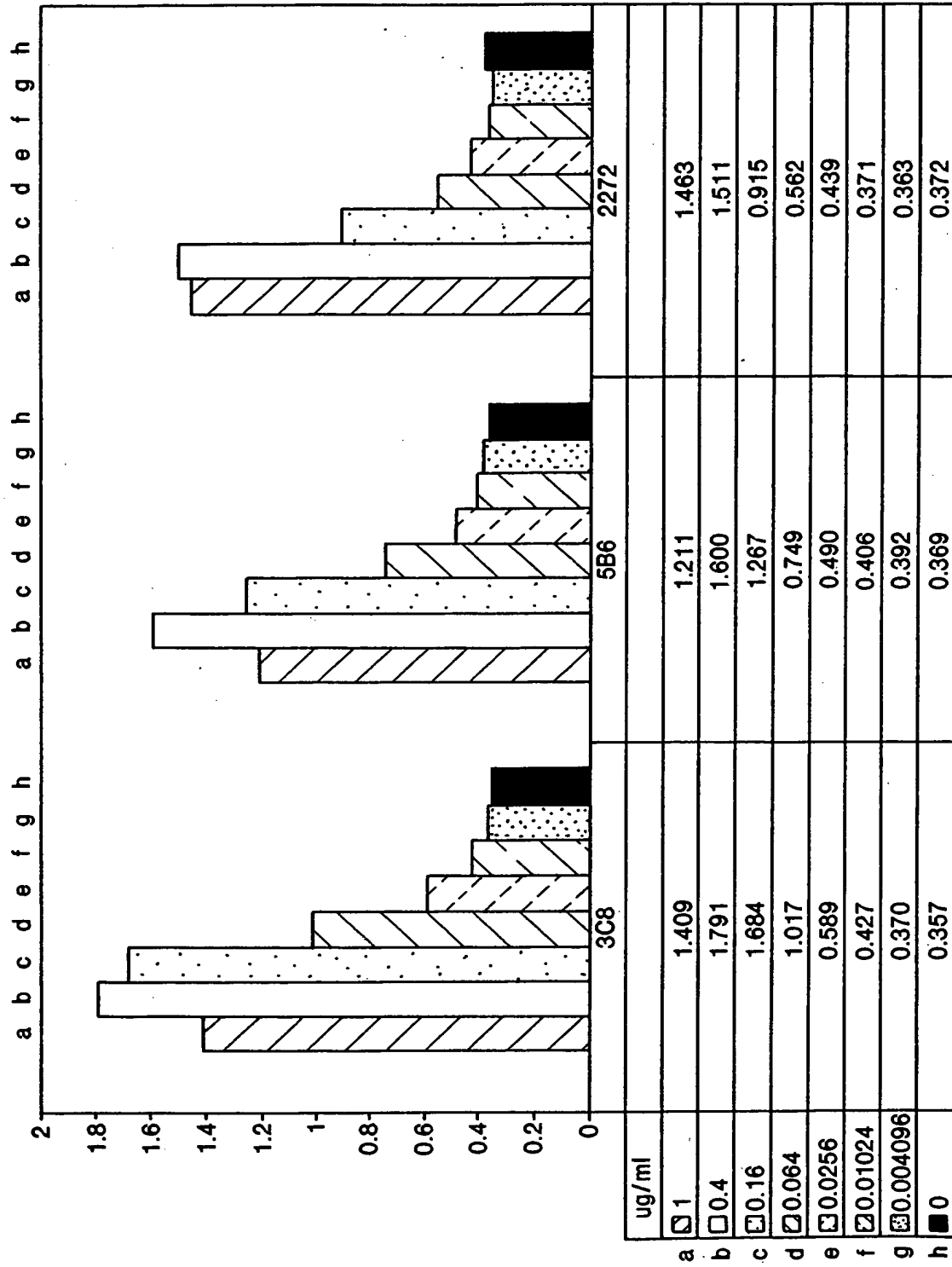


FIG. 13

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☒ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☒ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.